

SEQUENCE LISTING



<110> JENTSCH, Thomas J.

<120> NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
POTASSIUM CHANNELS

<130> 2818-1278

<140>

<141>

<160> 41

<170> PatentIn Ver. 2.1

<210> 1

<211> 2335

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(2335)

<220>

<221> CDS

<222> (33)..(2170)

<400> 1

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ggcccccagc cgggcgcgc cc atg gcc gag gcc ccc ccg cgc cgc ctc gcc 112
Met Ala Glu Ala Pro Pro Arg Arg Leu Gly
1 5 10

ctg ggt ccc ccg ccc ggg gac gcc ccc cgc gcg gag cta gtg gcg ctc 160
Leu Gly Pro Pro Pro Gly Asp Ala Pro Arg Ala Glu Leu Val Ala Leu
15 20 25

aag gcc gtg cag agc gaa cag gcc gag gcg gcc ggg gcc gcc tcc ccg 208
Thr Ala Val Gln Ser Glu Gln Gly Glu Ala Gly Gly Gly Ser Pro
30 35 40

cgc cgc ctc gcc ctc ctg gcc agc ccc ctg ccg ccg gcc gcg ccc ctc 256
Arg Arg Leu Gly Leu Leu Gly Ser Pro Leu Pro Pro Gly Ala Pro Leu
45 50 55

act ggg ggg ggg tac tac tac tac tac tac tac tac tac tac tac tac	114
Pro Gly Pro Gly Ser Gly Ser Gly Ser Ala Pys Gly Gln Arg Ser Ser	
60 60 70	
gac gag cac aag ggc tac cgc cgc cgc cgc cag aac tgg gtc tac aac gtc	352
Ala Ala His Lys Arg Tyr Arg Arg Leu Gln Asn Trp Val Tyr Asn Val	
75 80 85 90	
ctg gag cgg ccc cgc ggc tgg gcc ttc gtc tac cac gtc ttc ata ttc	400
Leu Glu Arg Pro Arg Gly Trp Ala Phe Val Tyr His Val Phe Ile Phe	
95 100 105	
ttg ctg gtc ttc agc tgc ctg gtc ctg ttc gtc ctg ttc act atc cag	448
Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Leu Ser Thr Ile Gln	
110 115 120	
gag cac cag gaa ctt gcc aac gag tgt ctc ctc atc ttg gaa ttc gtc	496
Glu His Gln Glu Leu Ala Asn Glu Cys Leu Leu Ile Leu Glu Phe Val	
125 130 135	
atg atc gtc gtt ttc gcc ttg gag tac atc gtc cgg gtc tgg tcc gcc	544
Met Ile Val Val Phe Gly Leu Glu Tyr Ile Val Arg Val Trp Ser Ala	
140 145 150	
gga tgc tgc tgc cgc tac cga gga tgg cag ggt cgc ttc cgc ttt gcc	592
Gly Cys Cys Cys Arg Tyr Arg Gly Trp Gln Gly Arg Phe Arg Phe Ala	
155 160 165 170	
aga aag ccc ttc tgt gtc atc gac ttc atc gtc ttc gtc gcc tcg gtc	640
Arg Lys Pro Phe Cys Val Ile Asp Phe Ile Val Phe Val Ala Ser Val	
175 180 185	
gcc gtc atc gcc ggc ggt acc cag gcc aac atc ttc gcc acg tcc gcg	688
Ala Val Ile Ala Ala Gly Thr Gln Gly Asn Ile Phe Ala Thr Ser Ala	
190 195 200	
ctg cgc agc atg cgc ttc ctg cag atc ctg cgc atg gtc cgc atg gac	736
Leu Arg Ser Met Arg Phe Leu Gln Ile Leu Arg Met Val Arg Met Asp	
205 210 215	
cgc cgc ggc ggc acc tgg aag ctg ctg gcc tca gtc gtc tac gcg cat	784
Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val Val Tyr Ala His	
220 225 230	
agc aag gag ctg atc acc gcc tgg tac atc ggg ttc ctg gtc ctc atc	832
Ser Lys Glu Leu Ile Thr Ala Trp Tyr Ile Gly Phe Leu Val Leu Ile	
235 240 245 250	

ttc gac tac ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc gac 971
 Phe Ala Ser Phe Leu Val Tyr Leu Ala Ala Lys Asp Ala Asn Ser Asp
 288 289 290

ttc ttc ttc ttc gac gac ttc ttc ttc ttc gac att aca ttc aca 972
 Phe Ser Ser Tyr Ala Asp Ser Leu Trp Trp Gly Thr Ile Thr Leu Thr
 271 272 273

acc atc ggc tat ggt gac aag aca cgc gac aca tgc ttc ggc agg gtc 973
 Thr Ile Gly Tyr Gly Asp Lys Thr Pro His Thr Trp Leu Gly Arg Val
 285 286 287

ctg gct gct ggc ttc gac tta ctg ggc atc tat ttc ttc gac ctg cct 1024
 Leu Ala Ala Gly Phe Ala Leu Leu Gly Ile Ser Phe Phe Ala Leu Pro
 300 301 302

gcc gcc atc cta gcc ttc gcc ttc gcc ctg aag gtc cag gag cag cac 1072
 Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val Gln Glu Gln His
 315 320 325 330

cgg cag aag cac ttc gag aag cgg agg atg cgc gca gcc aac ctc atc 1120
 Arg Gln Lys His Phe Glu Lys Arg Arg Met Pro Ala Ala Asn Leu Ile
 335 340 345

cag gct gcc tgg cgc ctg tac ttc acc gat atg agc cgg gcc tac ctg 1168
 Gln Ala Ala Trp Arg Leu Tyr Ser Thr Asp Met Ser Arg Ala Tyr Leu
 350 355 360

aca gcc acc tgc tac tac tat gac agt atc ctc cca ttc ttc aga gag 1216
 Thr Ala Thr Trp Tyr Tyr Tyr Asp Ser Ile Leu Pro Ser Phe Arg Glu
 365 370 375

ctg gcc ctc ttc ttc gag cac gtc caa cgg gcc cgc aat ggc ggc cta 1264
 Leu Ala Leu Leu Phe Glu His Val Gln Arg Ala Arg Asn Gly Gly Leu
 380 385 390

cgg ccc ctg gag gtc cgg cgg gcc cgc gta ccc gac gga gca ccc ttc 1312
 Arg Pro Leu Gln Val Arg Arg Ala Pro Val Pro Asp Gly Ala Pro Ser
 395 400 405 410

cgt tac cgc ccc gtt gcc acc tgc cac cgg cgc ggc agc acc ttc ttc 1360
 Arg Tyr Pro Pro Val Ala Thr Cys His Arg Pro Gly Ser Thr Ser Phe
 415 420 425

tgc cct ggc gaa agc agc cgg atg gcc atc aaa gac cgc atc cgc atg 1408
 Cys Pro Gly Glu Ser Ser Arg Met Gly Ile Lys Asp Arg Ile Arg Met
 430 435 440

ttt aat ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt	1460
Gly Ser Ser Ala Arg Arg Thr Gly Thr Ser Lys Gln Gln Leu Ala Phe	
445 487 487	
aca aca atg ccc acc tcc caa agc agc gag cag gtg ggt gag gac acc	1514
Pro Thr Met Pro Thr Ser Pro Ser Ser Glu Gln Val Gly Gln Ala Thr	
467 468 477	
agc ccc acc aag gtg caa aag agc tgg agc ttc aat gag cgc acc cgc	1552
Ser Pro Thr Lys Val Gln Lys Ser Trp Ser Phe Asn Asp Arg Thr Arg	
475 480 485 490	
ttc cgg gca tct ctg aga ctc aaa ccc cgc acc tct gct gag gat gcc	1600
Phe Arg Ala Ser Leu Arg Leu Lys Pro Arg Thr Ser Ala Glu Asp Ala	
495 500 505	
ccc tca gag gaa gta gca gag gag aag agc tac cag tgt gag ctc acg	1648
Pro Ser Glu Glu Val Ala Glu Glu Lys Ser Tyr Gln Cys Glu Leu Thr	
510 515 520	
gtg gac gac atc atg cct gct gtg aag aca gtc atc cgc tcc atc agg	1696
Val Asp Asp Ile Met Pro Ala Val Lys Thr Val Ile Arg Ser Ile Arg	
525 530 535	
att ctc aag ttc ctg gtg gcc aaa agg aaa ttc aag gag aca ctg cga	1744
Ile Leu Lys Phe Leu Val Ala Lys Arg Lys Phe Lys Glu Thr Leu Arg	
540 545 550	
cgc tac gac gtg aag gac gtc att gag cag tac tca gca ggc cac ctg	1792
Pro Tyr Asp Val Lys Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu	
555 560 565 570	
gac atg ctg ggc cgg atc aag agc ctg caa act cgg gtg gac caa att	1840
Asp Met Leu Gly Arg Ile Lys Ser Leu Gln Thr Arg Val Asp Gln Ile	
575 580 585	
gtg ggt cgg ggg ccc ggg gac agg aag gcc cgg gag aag ggc gac aag	1888
Val Gly Arg Gly Pro Gly Asp Arg Lys Ala Arg Glu Lys Gly Asp Lys	
590 595 600	
ggg ccc tcc gac gog gag gtg gtg gat gaa atc agc atg atg gga cgc	1936
Gly Pro Ser Asp Ala Glu Val Val Asp Glu Ile Ser Met Met Gly Arg	
605 610 615	
gtg gtc aag gtg gag aag cag gtg cag tcc atc gag cac aag ctg gac	1984
Val Val Lys Val Glu Lys Gln Val Gln Ser Ile Glu His Lys Leu Asp	
620 625 630	

140		150		160		170		180		190		200	
Arg Gly Trp	Gln Gly Arg	Ile Arg Phe	Ala Arg Lys	Ile Phe Tyr	Val								
	165		175		185								
Ile Asp Phe	Ile Val Phe	Val Ala Ser	Val Ala Val	Ile Ala Ala	Gly								
	195		205		215								
Thr Gln Gly	Asn Ile Phe	Ala Thr Ser	Ala Leu Arg	Ser Met Arg	Phe								
	225		235		245								
Leu Gln Ile	Leu Arg Met	Val Arg Met	Asp Arg Arg	Gly Gly Thr	Trp								
	255		265		275								
Lys Leu Leu	Gly Ser Val	Val Tyr Ala	His Ser Lys	Gln Leu Ile	Thr								
	285		295		305								
Ala Trp Tyr	Ile Gly Phe	Leu Val Leu	Ile Phe Ala	Ser Phe Leu	Val								
	315		325		335								
Tyr Leu Ala	Glu Lys Asp	Ala Asn Ser	Asp Phe Ser	Ser Tyr Ala	Asp								
	345		355		365								
Ser Leu Trp	Trp Gly Thr	Ile Thr Leu	Thr Thr Ile	Gly Tyr Gly	Asp								
	375		385		395								
Lys Thr Pro	His Thr Trp	Leu Gly Arg	Val Leu Ala	Ala Gly Phe	Ala								
	405		415		425								
Leu Leu Gly	Ile Ser Phe	Phe Ala Leu	Pro Ala Gly	Ile Leu Gly	Ser								
	435		445		455								
Gly Phe Ala	Leu Lys Val	Gln Glu Gln	His Arg Gln	Lys His Phe	Glu								
	465		475		485								
Lys Arg Arg	Met Pro Ala	Ala Asn Leu	Ile Gln Ala	Ala Trp Arg	Leu								
	495		505		515								
Tyr Ser Thr	Asp Met Ser	Arg Ala Tyr	Leu Thr Ala	Thr Trp Tyr	Tyr								
	525		535		545								
Tyr Asp Ser	Ile Leu Pro	Ser Phe Arg	Glu Leu Ala	Leu Leu Phe	Glu								
	555		565		575								
His Val Gln	Arg Ala Arg	Asn Gly Gly	Leu Arg Pro	Leu Gln Val	Arg								
	585		595		605								
Arg Ala Pro	Val Pro Asp	Gly Ala Pro	Ser Arg Tyr	Pro Pro Val	Ala								
	615		625		635								
Thr Lys His	Arg Pro Gly	Ser Thr Ser	Phe Cys Pro	Gly Glu Ser	Ser								
	645		655		665								
Arg Met Gly	Ile Lys Asp	Arg Ile Arg	Met Gly Ser	Ser Glu Arg	Arg								
	675		685		695								
Thr Gly Pro	Ser Lys Gln	Gln Leu Ala	Pro Pro Thr	Met Pro Thr	Ser								
	705		715		725								
Pro Ser Ser	Glu Gln Val	Gly Glu Ala	Thr Ser Pro	Thr Lys Val	Gln								
	735		745		755								
Lys Ser Trp	Ser Phe Asn	Asp Arg Thr	Arg Phe Arg	Ala Ser Leu	Arg								
	765		775		785								
Leu Lys Pro	Arg Thr Ser	Ala Glu Asp	Ala Pro Ser	Glu Glu Val	Ala								
	795		805		815								
Glu Glu Lys	Ser Tyr Gln	Cys Glu Leu	Thr Val Asp	Asp Ile Met	Pro								
	825		835		845								
Ala Val Lys	Thr Val Ile	Arg Ser Ile	Arg Ile Leu	Lys Phe Leu	Val								

Ala	Lys	Arg	Lys	Phe	Lys	Gln	Thr	Leu	Arg	Pro	Tyr	Asp	Val	Lys	Asp
545					557					568					571
Val	Ile	Gln	Gln	Tyr	Ser	Ala	Gly	His	Leu	Asp	Met	Leu	Gly	Arg	Ile
				568					571						573
Lys	Ser	Leu	Gln	Thr	Arg	Val	Asp	Gln	Ile	Val	Gly	Arg	Gly	Pro	Gly
				580					583					590	
Asp	Arg	Lys	Ala	Arg	Gln	Lys	Gly	Asp	Lys	Gly	Pro	Ser	Asp	Ala	Gln
		595					600						605		
Val	Val	Asp	Gln	Ile	Ser	Met	Met	Gly	Arg	Val	Val	Lys	Val	Gln	Lys
	610					615					620				
Gln	Val	Gln	Ser	Ile	Gln	His	Lys	Leu	Asp	Leu	Leu	Leu	Gly	Phe	Tyr
625					630					635					640
Ser	Arg	Cys	Leu	Arg	Ser	Gly	Thr	Ser	Ala	Ser	Leu	Gly	Ala	Val	Gln
				645					650						655
Val	Pro	Leu	Phe	Asp	Pro	Asp	Ile	Thr	Ser	Asp	Tyr	His	Ser	Pro	Val
			660					665					670		
Asp	His	Gln	Asp	Ile	Ser	Val	Ser	Ala	Gln	Thr	Leu	Ser	Ile	Ser	Arg
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Ser	Val	Ser	Thr	Asn	Met	Asp									
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<212> tNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 3

catgggtctc tgagcgcccc gaggc

24

<210> 4

<211> 14

<212> tNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 4

aggcaggtc tgcgcgggga aacg

24

<210> 5
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 5
cagcagag ctgaactcc agg 23

<210> 6
<211> 21
<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR Primer

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aacctgtctc ctgagccatg g 21

<210> 7
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 7
actgggtccg cgctgtgacc 20

<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 8
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<211 > 4
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<221 >
<223 > Description of Artificial Sequence: PCR Primer

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<213 > Artificial Sequence

<220 >
<223 > Description of Artificial Sequence: PCR Primer

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<211 > 21
<212 > DNA
<213 > Artificial Sequence

<220 >
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<400 > 11
atccctttcc cgtgtggaag c 21

<210 > 12
<211 > 21
<212 > DNA
<213 > Artificial Sequence

<220 >
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<400 > 12
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<210 > 12
<211 > 11
<212 > DNA
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<220 >
<223 > Description of Artificial Sequence: PCR Primer

<400 > 13
ctctatgata aggttctctac c

11

<210 > 14
<211 > 19
<212 > DNA
<213 > Artificial Sequence

<220 >
<223 > Description of Artificial Sequence: PCR Primer

<400 > 14
atgtgtgaca ggggtgagc

19

<210 > 15
<211 > 20
<212 > DNA
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<220 >
<223 > Description of Artificial Sequence: PCR Primer

<400 > 15
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<210 > 16
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<212 > DNA
<213 > Artificial Sequence

<220 >
<223 > Description of Artificial Sequence: PCR Primer

<400 > 16
acacagggtt gacacacc

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<220>
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<400> 17
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<210> 18
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<220>
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<400> 18
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21

<210> 19
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<213> Artificial Sequence

<220>
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<400> 19
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<210> 20
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<220>
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<211> 21
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<220>
<223> Description of Artificial Sequence: PCR Primer

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<210> 22
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<220>
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<400> 22
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<210> 23
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<220>
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<400> 23
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<210> 24
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<220>
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<220>
<221> Description of Artificial Sequence: PCR Primer

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<220>
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<400> 26
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<210> 27
<211> 21
<212> DNA
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<220>
<221> Description of Artificial Sequence: PCR Primer

<400> 17
atgattctc ctccatcagg c 21

<210> 28
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<220>
<221> Description of Artificial Sequence: PCR Primer

<400> 28
aacgcatact ccccatgtca 20

<210> 21
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<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 29
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21

<210> 30
<211> 24
<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 30
tgtgaggag tgagttcaag tacg

24

<210> 31
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 31
agtactgat ggagcgccct ctcg

24

<210> 32
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<220>
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<400> 32
tcattccacg taagtcaca ctgg

24

4110> 10
 4111> 60
 4112> 85
 4113> Homo sapiens

4110> 10

Met Ala Ala Ala Ser Ser Pro Pro Arg Ala Gly Arg Lys Arg Trp Gly
 1 5 10 15

Trp Gly Arg Leu Pro Gly Ala Arg Arg Gly Ser Ala Gly Leu Ala Lys
 20 25 30

Lys Cys Pro Phe Ser Leu Glu Leu Ala Glu Gly Gly Pro Ala Gly Gly
 35 40 45

Ala Leu Tyr Ala Pro Ile Ala Pro Gly Ala Pro Gly Pro Ala Pro Pro
 50 55 60

Ala Ser Pro Ala Ala Pro Ala Ala Pro Pro Val Ala Ser Asp Leu Gly
 65 70 75 80

Pro Arg Pro Pro Val Ser Leu Asp Pro Arg Val Ser Ile Tyr Ser Thr
 85 90 95

Arg Arg Pro Val Leu Ala Arg Thr His Val Gln Gly Arg Val Tyr Asn
 100 105 110

Phe Leu Glu Arg Pro Thr Gly Trp Lys Cys Phe Val Tyr His Phe Ala
 115 120 125

Val Phe Leu Ile Val Leu Val Cys Leu Ile Phe Ser Val Leu Ser Thr
 130 135 140

Ile Glu Gln Tyr Ala Ala Leu Ala Thr Gly Thr Leu Phe Trp Met Glu
 145 150 155 160

Ile Val Leu Val Val Phe Phe Gly Thr Glu Tyr Val Val Arg Leu Trp
 165 170 175

Ser Ala Gly Cys Arg Ser Lys Tyr Val Gly Leu Trp Gly Arg Leu Arg
 180 185 190

Phe Ala Arg Lys Pro Ile Ser Ile Ile Asp Leu Ile Val Val Val Ala
 195 200 205

Ser Met Val Val Leu Cys Val Gly Ser Lys Gly Gln Val Phe Ala Thr
 210 215 220

Ser Ala Ile Arg Gly Ile Arg Ile Leu Gln Ile Leu Arg Met Ile His
 111 121 131 141

Val Asp Arg Gln Gly Gly Thr Trp Arg Leu Leu Gly Ser Val Val Phe
 145 155 165

Ile His Arg Gln Glu Leu Ile Thr Thr Leu Tyr Ile Gly Phe Leu Gly
 171 181 191

Leu Ile Phe Ser Ser Tyr Phe Val Tyr Leu Ala Glu Lys Asp Ala Val
 205 215 225

Asn Glu Ser Gly Arg Val Glu Phe Gly Ser Tyr Ala Asp Ala Leu Trp
 230 245 255

Trp Gly Val Val Thr Val Thr Thr Ile Gly Tyr Gly Asp Lys Val Pro
 265 275 285

Gln Thr Trp Val Gly Lys Thr Ile Ala Ser Cys Phe Ser Val Phe Ala
 295 305 315

Ile Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala
 320 330 340

Leu Lys Val Gln Gln Lys Gln Arg Gln Lys His Phe Asn Arg Gln Ile
 355 365 375

Pro Ala Ala Ala Ser Leu Ile Gln Thr Ala Trp Arg Cys Tyr Ala Ala
 385 395 405

Glu Asn Pro Asp Ser Ser Thr Trp Lys Ile Tyr Ile Arg Lys Ala Pro
 415 425 435

Arg Ser His Thr Leu Leu Ser Pro Ser Pro Lys Pro Lys Lys Ser Val
 445 455 465

Val Val Lys Lys Lys Lys Phe Lys Leu Asp Lys Asp Asn Gly Val Thr
 475 485 495

Pro Gly Glu Lys Met Leu Thr Val Pro His Ile Thr Cys Asp Pro Pro
 505 515 525

Glu Glu Arg Arg Leu Asp His Phe Ser Val Asp Gly Tyr Asp Ser Ser
 535 545 555

Val Arg Lys Ser Pro Thr Leu Leu Glu Val Ser Met Pro His Phe Met
 565 575 585

Arg Thr Asn Ser Phe Ala Ala Arg Leu Arg Leu Glu Gly Ala Thr Leu
470 475 480

Leu Thr Pro Ile Thr His Ile Ser Gln Leu Arg Gln His His Arg Ala
500 505 510

Thr Ile Lys Val Ile Arg Arg Met Gln Tyr Phe Val Ala Lys Lys Lys
515 520 525

Phe Gln Gln Ala Arg Lys Pro Tyr Asp Val Arg Asp Val Ile Gln Gln
530 535 540

Tyr Ser Gln Gly His Leu Asn Leu Met Val Arg Ile Lys Glu Leu Gln
545 550 555 560

Arg Arg Leu Asp Gln Ser Ile Gly Lys Pro Ser Leu Phe Ile Ser Val
565 570 575

Ser Glu Lys Ser Lys Asp Arg Gly Ser Asn Thr Ile Gly Ala Arg Leu
580 585 590

Asn Arg Val Glu Asp Lys Val Thr Gln Leu Asp Gln Arg Leu Ala Leu
595 600 605

Ile Thr Asp Met Leu His Gln Leu Leu Ser Leu His Gly Gly Ser Thr
610 615 620

Pro Gly Ser Gly Gly Pro Pro Arg Glu Gly Gly Ala His Ile Thr Gln
625 630 635 640

Pro Cys Gly Ser Gly Gly Ser Val Asp Pro Glu Leu Phe Leu Pro Ser
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Asn Thr Leu Pro Thr Tyr Glu Gln Leu Thr Val Pro Arg Arg Gly Pro
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Asp Glu Gly Ser
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<210> 34

<211> 844

<212> PRT

<213> Homo sapiens

<400> 34

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Ala Lys Lys Leu Lys Val Gly Ile Val Gly Leu Asp Phe Gly Ala Pro
 21 38 41

Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
 35 41 45

Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
 51 55 61

Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Glu Asn Phe
 65 70 75 80

Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
 85 90 95

Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
 100 105 110

Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
 115 120 125

Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
 130 135 140

Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
 145 150 155 160

Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
 165 170 175

Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
 180 185 190

Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
 195 200 205

Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
 210 215 220

Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe
 225 230 235 240

Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly
 245 250 255

Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
 260 265 270

Ile Thr Leu Thr Thr Ile Gly Tyr Arg Asp Lys Tyr Pro Ala Thr Arg
 378 387 396

Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
 391 398 407

Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
 413 420 429

Gln Gln Gln His Arg Gln Lys His Phe Gln Lys Arg Arg Asn Pro Ala
 435 444 453

Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
 458 467 476

Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
 481 490 500

Val Pro Met Tyr Arg Leu Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu
 505 514 523

Arg Asn Leu Lys Ser Lys Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro
 528 537 546

Pro Glu Pro Ser Pro Ser Gln Lys Val Ser Leu Lys Asp Arg Val Phe
 551 560 569

Ser Ser Pro Arg Gly Val Ala Ala Lys Gly Lys Gly Ser Pro Gln Ala
 574 583 592

Gln Thr Val Arg Arg Ser Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser
 597 606 615

Pro Ser Lys Val Pro Lys Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala
 620 629 638

Arg Gln Ala Phe Arg Ile Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu
 643 652 661

Glu Ala Ser Leu Pro Gly Glu Asp Ile Val Asp Asp Lys Ser Cys Pro
 666 675 684

Cys Glu Phe Val Thr Glu Asp Leu Thr Pro Gly Leu Lys Val Ser Ile
 689 698 707

Arg Ala Val Cys Val Met Arg Phe Leu Val Ser Lys Arg Lys Phe Lys
 712 721 730

Val Ser Leu Arg Pro Tyr Asp Val Met Asp Val Ile Gln Gln Tyr Ser
581 585 589

Ala Gly His Leu Asp Met Leu Ser Arg Ile Lys Ser Leu Gln Ser Arg
590 594 598 602

Val Asp Gln Ile Val Gly Arg Gly Pro Ala Ile Thr Asp Lys Asp Arg
603 607 611 615

Thr Lys Gly Pro Ala Glu Ala Glu Leu Pro Gln Asp Pro Ser Met Met
620 624 628 632

Gly Arg Leu Gly Lys Val Glu Lys Gln Val Leu Ser Met Glu Lys Lys
635 639 643 647

Leu Asp Phe Leu Val Asn Ile Tyr Met Gln Arg Met Gly Ile Pro Pro
650 654 658 662

Thr Glu Thr Glu Ala Tyr Phe Gly Ala Lys Glu Pro Glu Pro Ala Pro
665 669 673 677 681

Pro Tyr His Ser Pro Glu Asp Ser Arg Glu His Val Asp Arg His Gly
684 688 692 696 700

Cys Ile Val Lys Ile Val Arg Ser Ser Ser Ser Thr Gly Gln Lys Asn
703 707 711 715 719

Phe Ser Ala Pro Pro Ala Ala Pro Pro Val Gln Cys Pro Pro Ser Thr
722 726 730 734 738

Ser Trp Gln Pro Gln Ser His Pro Arg Gln Gly His Gly Thr Ser Pro
741 745 749 753 757

Val Gly Asp His Gly Ser Leu Val Arg Ile Pro Pro Pro Pro Ala His
760 764 768 772 776

Glu Arg Ser Leu Ser Ala Tyr Gly Gly Gly Asn Arg Ala Ser Met Glu
779 783 787 791 795

Phe Leu Arg Gln Glu Asp Thr Pro Gly Cys Arg Pro Pro Glu Gly Thr
798 802 806 810 814

Leu Arg Asp Ser Asp Thr Ser Ile Ser Ile Pro Ser Val Asp His Glu
817 821 825 829 833

Glu Leu Glu Arg Ser Phe Ser Gly Phe Ser Ile Ser Gln Ser Lys Glu
836 840 844 848 852

Asn Leu Asp Ala Leu Asn Ser Cys Tyr Ala Ala Val Ala Pro Cys Ala
 715 720 725 730

Lys Val Arg Pro Tyr Ile Ala Glu Gly Glu Ser Asp Thr Asp Ser Asp
 735 740 745 750

Leu Cys Thr Pro Cys Gly Pro Pro Pro Arg Ser Ala Thr Gly Glu Gly
 755 760 765 770

Pro Phe Gly Asp Val Gly Trp Ala Gly Pro Arg Lys
 775 780

42100 35

42110 872

42120 FRT

42130 Homo sapiens

44000 35

Met Gly Leu Lys Ala Arg Arg Ala Ala Gly Ala Ala Gly Gly Gly Gly
 1 5 10 15

Asp Gly Gly Gly Gly Gly Gly Gly Ala Ala Asn Pro Ala Gly Gly Asp
 20 25 30

Ala Ala Ala Ala Gly Asp Glu Glu Arg Lys Val Gly Leu Ala Pro Gly
 35 40 45

Asp Val Glu Gln Val Thr Leu Ala Leu Gly Ala Gly Ala Asp Lys Asp
 50 55 60

Gly Thr Leu Leu Leu Glu Gly Gly Gly Arg Asp Glu Gly Gln Arg Arg
 65 70 75 80

Thr Pro Gln Gly Ile Gly Leu Leu Ala Lys Thr Pro Leu Ser Arg Pro
 85 90 95

Val Lys Arg Asn Asn Ala Lys Tyr Arg Arg Ile Gln Thr Leu Ile Tyr
 100 105 110

Asp Ala Leu Glu Arg Pro Arg Gly Trp Ala Leu Leu Tyr His Ala Leu
 115 120 125

Val Phe Leu Ile Val Leu Gly Cys Leu Ile Leu Ala Val Leu Thr Thr
 130 135 140

Phe Lys Glu Tyr Glu Thr Val Ser Gly Asp Trp Leu Leu Leu Leu Glu

141 Thr Phe Ala Ile Ile Ile Phe Gly Ala Ala Phe Ala Leu Arg Ile Trp
 165 170 175
 Ala Ala Gly Cys Cys Cys Arg Tyr Lys Gly Trp Arg Gly Arg Leu Lys
 180 185 190
 Phe Ala Arg Lys Pro Leu Cys Met Leu Asp Ile Phe Val Leu Ile Ala
 195 200 205
 Ser Val Pro Val Val Ala Val Gly Asn Gln Gly Asn Val Leu Ala Thr
 210 215 220
 Ser Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met Leu Arg Met
 225 230 235 240
 Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Ala Ile Cys Ala
 245 250 255
 His Ser Lys Glu Leu Ile Thr Ala Trp Tyr Ile Gly Phe Leu Thr Leu
 260 265 270
 Ile Leu Ser Ser Phe Leu Val Tyr Leu Val Glu Lys Asp Val Pro Glu
 275 280 285
 Val Asp Ala Gln Gly Glu Glu Met Lys Glu Glu Phe Glu Thr Tyr Ala
 290 295 300
 Asp Ala Leu Trp Trp Gly Leu Ile Thr Leu Ala Thr Ile Gly Tyr Gly
 305 310 315 320
 Asp Lys Thr Pro Lys Thr Trp Glu Gly Arg Leu Ile Ala Ala Thr Phe
 325 330 335
 Ser Leu Ile Gly Val Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly
 340 345 350
 Ser Gly Leu Ala Leu Lys Val Gln Glu Gln His Arg Gln Lys His Phe
 355 360 365
 Glu Lys Arg Arg Lys Pro Ala Ala Glu Leu Ile Gln Ala Ala Trp Arg
 370 375 380
 Tyr Tyr Ala Thr Asn Pro Asn Arg Ile Asp Leu Val Ala Thr Trp Arg
 385 390 395 400
 Phe Tyr Glu Ser Val Val Ser Phe Pro Phe Phe Arg Lys Glu Gln Leu

411 Ala Ala Ser Ser Glu Lys Leu Gly Leu Leu Asp Arg Val Arg Leu
 421 438 451

Ser Asn Pro Arg Gly Ser Asn Thr Lys Gly Lys Leu Phe Thr Pro Leu
 435 441 445

Asn Val Asp Ala Ile Glu Glu Ser Pro Ser Lys Glu Pro Lys Pro Val
 450 455 461

Gly Leu Asn Asn Lys Glu Arg Phe Arg Thr Ala Phe Arg Met Lys Ala
 465 470 475 480

Tyr Ala Phe Trp Gln Ser Ser Glu Asp Ala Gly Thr Gly Asp Pro Met
 485 490 495

Ala Glu Asp Arg Gly Tyr Gly Asn Asp Phe Pro Ile Glu Asp Met Ile
 500 505 510

Pro Thr Leu Lys Ala Ala Ile Arg Ala Val Arg Ile Leu Gln Phe Arg
 515 520 525

Leu Tyr Lys Lys Lys Phe Lys Glu Thr Leu Arg Pro Tyr Asp Val Lys
 530 535 540

Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met Leu Ser Arg
 545 550 555 560

Ile Lys Tyr Leu Gln Thr Arg Ile Asp Met Ile Phe Thr Pro Gly Pro
 565 570 575

Pro Ser Thr Pro Lys His Lys Lys Ser Gln Lys Gly Ser Ala Phe Thr
 580 585 590

Phe Pro Ser Gln Gln Ser Pro Arg Asn Glu Pro Tyr Val Ala Arg Pro
 595 600 605

Ser Thr Ser Glu Ile Glu Asp Gln Ser Met Met Gly Lys Phe Val Lys
 610 615 620

Val Glu Arg Gln Val Gln Asp Met Gly Lys Lys Leu Asp Phe Leu Val
 625 630 635 640

Asp Met His Met Gln His Met Glu Arg Leu Gln Val Gln Val Thr Glu
 645 650 655

Tyr Tyr Pro Thr Lys Gly Thr Ser Ser Pro Ala Glu Ala Glu Lys Lys

Glu Asp Asn Arg Tyr Ser Asp Leu Lys Thr Ile Ile Lys Asn Tyr Ser
678 681 685

Glu Thr Gly Pro Pro Glu Pro Pro Tyr Ser Phe His Glu Val Thr Ile
691 695 700

Asp Lys Val Ser Pro Tyr Gly Phe Phe Ala His Asp Pro Val Asn Leu
705 710 715 720

Pro Arg Gly Gly Pro Ser Ser Gly Lys Val Gln Ala Thr Pro Pro Ser
725 730 735

Ser Ala Thr Thr Tyr Val Glu Arg Pro Thr Val Leu Pro Ile Leu Thr
740 745 750

Leu Leu Asp Ser Arg Val Ser Cys His Ser Gln Ala Asp Leu Gln Gly
755 760 765

Pro Tyr Ser Asp Arg Ile Ser Pro Arg Gln Arg Arg Ser Ile Thr Arg
770 775 780

Asp Ser Asp Thr Pro Leu Ser Leu Met Ser Val Asn His Glu Glu Leu
785 790 795 800

Glu Arg Ser Pro Ser Gly Phe Ser Ile Ser Gln Asp Arg Asp Asp Tyr
805 810 815

Val Phe Gly Pro Asn Gly Gly Ser Ser Trp Met Arg Glu Lys Arg Tyr
821 825 830

Leu Ala Glu Gly Glu Thr Asp Thr Asp Thr Asp Pro Phe Thr Pro Ser
835 840 845

Gly Ser Met Pro Leu Ser Ser Thr Gly Asp Gly Ile Ser Asp Ser Val
850 855 860

Trp Thr Pro Ser Asn Lys Pro Ile
865 870

(210): 36

(211): 21

(212): DNA

(213): Artificial Sequence

(220):

<210> Description of Artificial Sequence: PCR Primer

<400> 36

agggtgggat cagtcattg g

21

<210> 37

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 37

aggtagggcag gctgttgctg g

21

<210> 38

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 38

gacatgggcac ctcccccgctg g

21

<210> 39

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 39

ccctctccaa tctagggcct gac

23

<210> 40

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of Artificial Sequence: PCR Primer

<411> 4

caagggaatg aacatattgt agac

24

<211> 41

<211> 14

<212> DNA

<213> Artificial Sequence

<221>

<223> Description of Artificial Sequence: PCR Primer

<400> 41

cagaagagtc aagatgggca ggac

24